16. (Twice Amended) A method of making a microsphere array comprising:

a) contacting a substrate with a surface comprising discrete sites at a density of at least 100 sites per 1 mm^2, with a solution comprising a population of different particles, wherein said particles do not comprise an optical signature; and

b) applying energy to said substrate or said solution, or both, such that at least a subpopulation of said different particles randomly associate onto sites.

The following claims are new:

36. (New) A method for decoding an array composition comprising:

a) providing an array comprising:

i) substrate with a surface comprising discrete sites at a density of at least 100 sites per 1 mm^2, wherein said sites are wells; and

ii) a population of microspheres randomly distributed on said sites, wherein said population comprises at least a first and a second subpopulation each comprising a different bioactive agent and do not comprise a label; and

c) decoding a location of said bioactive agent by correlating said bioactive agent with said location.

37. (New) The method according to claim 36, wherein said bioactive agents are nucleic acids.

38. (New) The method according to claim 37, wherein said nucleic acids are DNA.

39. (New) The method according to claim 37, wherein said nucleic acids are single stranded nucleic acids.

40. (New) The method according to claim 37, wherein said nucleic acids are double stranded nucleic acids.

41. (New) The method according to claim 36, wherein said bioactive agents are proteins.

42. (New) The method according to claim 36, wherein said substrate is a fiber optic bundle.

43. (New) The method according to claim 36, wherein said substrate is glass.

44. (New) The method according to claim 36, wherein said substrate is plastic.

45. (New) The method according to claim 36, 37, 38, 39, 40, 41, 41, 43 or 44, whereby said decoding comprises contacting said array with at least first and second different decoder binding ligands, whereby said first and second decoder binding ligands bind to first and second bioactive

agents, respectively, to thereby identify a location of said first and second bioactive agents to thereby decode said array.

46. (New) The method according to claim 45, wherein said first and second decoder binding ligand comprise first and second different labels.

47. (New) The method according to claim 36, 37, 38 or 38, whereby said decoding comprises contacting said array with at least a first and second different nucleic acid decoder binding ligand, whereby said first and second different nucleic acid decoder binding ligand hybridizes with said first and second bioactive agents, respectively, to thereby identify a location of said frist and second bioactive agents to thereby decode said array.

48. (New) The method according to claim 36, 37, 38, 39, 40, 41, 42, 43 or 44, wherein each subpopulation further comprises a different identifier binding ligand.

49. (New) The method according to claim 48, whereby said decoding comprises contacting said array with at least first and second different decoder binding ligands, whereby said first and second decoder binding ligands bind to a first and second identifier binding ligand, whereby said first and second identifier binding ligand identifies said first and second bioactive agent, respectively, to thereby identify a location of said first and second bioactive agents to thereby decode said array.

50. (New) The method according to claim 49, wherein said first and second decoder binding ligands comprise first and second labels.

51. (New) The method according to claim 49, whereby said first and second different identifier binding ligands are different nucleic acids and said first and second decoder binding ligands are nucleic acids that hybridize to said first and second identifier binding ligands, respectively.

52. (New) A method for decoding an array composition comprising:

a) providing an array comprising:

i) substrate with a surface comprising discrete sites at a density of at least 100 sites per 1 mm^2, wherein said sites are wells; and

ii) a population of microspheres randomly distributed on said sites, wherein said population comprises at least a first and a second subpopulation each comprising:

a. a different bioactive agent; and

b. a different identifier binding ligand; and

b) decoding a location of said bioactive agent by correlating said bioactive agent with said location.

53. (New) The method according to claim 52, whereby said decoding comprises contacting said array with at least first and second different decoder binding ligands, whereby said first and second decoder binding ligands bind to said first and second identifier binding ligand, whereby said first and second identifier binding ligand identifies said first and second bioactive agent, respectively, to thereby identify a location of said first and second bioactive agents to thereby decode said array.

54. (New) A method of determining the presence of a target analyte in a sample comprising:

a) contacting said sample with an array comprising:

i) substrate with a surface comprising discrete sites at a density of at least 100 sites per 1 mm^2, wherein said sites are wells; and

ii) a population of microspheres randomly distributed on said sites, wherein said population comprises at least a first and a second subpopulation each comprising a different bioactive agent and do not comprise a label;

b) determining the presence or absence of said target analyte; and

c) decoding a location of said bioactive agent by correlating said bioactive agent with said location.

55. (New) The method according to claim 54, wherein said decoding comprises contacting said array with at least first and second different decoder binding ligands, whereby said first and second decoder binding ligands bind to first and second bioactive agents, respectively, to thereby identify a location of said first and second bioactive agents to thereby decode said array.

56. (New) The method according to claim 54, wherein each subpopulation further comprises a different identifier binding ligand.

57. (New) The method according to claim 56, whereby said decoding comprises contacting said array with at least first and second different decoder binding ligands, whereby said first and second decoder binding ligands bind to a first and second identifier binding ligand, whereby said first and second identifier binding ligand identifies said first and second bioactive agent, respectively, to thereby identify a location of said first and second bioactive agents to thereby decode said array.

58. (New) A method of determining the presence of a target analyte in a sample comprising:

a) contacting said sample with an array comprising:

i) substrate with a surface comprising discrete sites at a density of at least 100 sites per 1 mm^2, wherein said sites are wells; and

ii) a population of microspheres randomly distributed on said sites, wherein said population comprises at least a first and a second subpopulation each comprising:

a. a different bioactive agent; and

b. a different identifier binding ligand;

b) determining the presence or absence of said target analyte; and

c) decoding a location of said bioactive agent by correlating said bioactive agent with said location.

59. (New) The method according to claim 60, whereby said decoding comprises contacting said array with at least first and second different decoder binding ligands, whereby said first and second decoder binding ligands bind to a first and second identifier binding ligand, whereby said first and second identifier binding ligand identifies said first and second bioactive agent, respectively, to thereby identify a location of said first and second bioactive agents to thereby decode said array.

REMARKS

Claims 8-14 and 21-35 have been canceled. Claim 16 is amended. Support for this amendment is found at p. 6, line 25 to p. 7, line 2. Claims 36-59 have been newly added. For the Examiner's convenience, a copy of the currently pending claims is attached hereto as Appendix A. A copy of the "Version to Show Changes Made" is also attached as Appendix B. Support for newly added claims 36-59 can be found in the originally filed claims as well as in the